

Figure 1

Nucleotide sequence of ATCC21529 ask (SEQ ID NO:1)

1 GTGGCCCTGC TCGTACAGAA ATATGCCGTT TCCTCGCTTG AGAGTGCGGA
51 ACGCATTAGA AACGTCGCTG AACGGATCGT TGCCACCAAG AAGGCTGGAA
101 ATGATGTCGT GGTTGTCTGC TCCGCAATGG GAGACACCAC GGATGAACCT
151 CTAGAACTTG CAGCGGCAGT GAATCCCATT CGGCCAGCTC GTGAAATGGA
201 TATGCTCCTG ACTGCTGGTG AGCGTATTTC TAACGCTCTC GTCGCCATGG
251 CTATTGAGTC CCTTGGCGCA GAAGCTCAAT CTTCACTGG CTCTCAGGCT
301 GGTGTGCTCA CCACCCGAGCG CCACGGAAAC GCACCCATTG TTGACGTAC
351 ACCGGGTCTG GTGCGTGAAG CACTCGATGA GGGCAAGATC TGCATTGTTG
401 CTGGTTTCA GGGTGTAAAT AAAGAACCCC GCGATGTCAC CACGGTGGGT
451 CGTGGTGGTT CTGACACCAAC TGCAGTTGCG TTGGCAGCTG CTTTGAACGC
501 TGATGTGTGT GAGATTTACT CGGACGTTGA CGGTGTGTAT ACCGCTGACC
551 CGCGCATCGT TCCTAATGCA CAGAARGCTGG AAAAGCTCAG CTTCGAAGAA
601 ATGCTGGAAC TTGCTGCTGT TGGCTCCAAG ATTTGGTGC TGCAGTGT
651 TGAATACGCT CGTGCATTCA ATGTGCCACT TGGCGTACGC TCGTCTTATA
701 GTAATGATCC CGGGCACTTG ATTGCCGGCT CTATGGAGGA TATTCTGTG
751 GAAGAAGCAG TCCTTACCCG TGTCGCAACC GACAAGTCCG AAGCCAAAGT
801 AACCGTTCTG GGTATTTCCG ATAAGCCAGG CGAGGCTGCC AAGGTTTCC
851 GTGGCTTGGC TGATGCAGAA ATCACACATTG ACATGGTTCT GCAGAACGTC
901 TCCTCTGTGG AAGACGGCAC CACCGACATC ACCTTCACCT GCCCTCGCGC
951 TGACGGACGC CGTGCAGATGG AGATCTTGAA GAAGCTTCAG GTTCAGGGCA
1001 ACTGGACCAA TGTGTTTAC GACGACCAGG TCGGCAAAGT CTCCCTCGTG
1051 GGTGCTGGCA TGAAGTCTCA CCCAGGTGTT ACCGCGAGGT TCATGGAAGC
1101 TCTGCGCGAT GTCAACGTGA ACATCGAATT GATTCATC TCTGAGATCC
1151 GCATTTCCGT GCTGATCCGT GAAGATGATC TGGATGCTGC TGCACGTGCA
1201 TTGCATGAGC AGTTCCAGCT GGGCGCGAA GACGAAGCCG TCGTTTATGC
1251 AGGCACCGGA CGCTAA

Fig. 2

06/22/11 - 11/28/00

097244-112800

SEQ ID NO: 2

Proline amino acid sequence of ATCC 21529 alk.

1 61
GTCGCCCTGGTGGTACAGAAATATGGGGTTCTGGTGGAGAGTGGGGAGCATTAGA
2 60
E A L V V O N K Y G C S S I E S A E P I R
3 61
AAGCTCGCTGAACGGATCGTTGCCACCAAGAAGGCTCGAAATGATCTCGTGGTCTCTGC
120
N V A E R I V A T K K A G N D V V V V C
4 121
TCGGCAATGGGAGACACCCACGGATGAACCTCTAGAACCTTGAGCCGGAGTGAATCCCGTT
180
S A M G D T T D E L L E L A A A V N P V
5 181
CCGCCAGCTCGTGAATGGATATGCTCTGACTGCTGGTAGACGTATTCTAACGCTCTC
240
P P A R E M D M L L T A G E R I S N A L
6 241
GTCGCCATGGCTATTGAGTCCCTGGCCAGAAGCTCACTTCACTGGCTCTCAGGCT
300
V A M A I E S L G A E A Q S F T G S Q A
7 301
GGTGTGCTCACCAACCGAGCGCCACGGAAACGCACGCATTGTTGACCTCACACCGGGTCGT
360
G V L T T E R H G N A R I V D V T P G R
8 361
GTGCGTGAAGCACTCGATGGGCAAGATCTGCATTGTTGCTGGTTTCAGGGTGTAAAT
420
V R E A L D E G K I C I V A G F Q G V N
9 421
AAAGAAAACCCCGCGATGTCACCACTGGGGCTGCTGGTTCTGACACCCTGCAGTTGCG
480
K E T R D V T T L G R G G S D T T A V A
10 481
TTGGCAGCTGCTTGAAACGCTGATGTTGAGATTACTCGGACGTTGACGGTGTGTAT
540
L A A A L N A D V C E I Y S D V D G V Y
11 541
ACCGCTGACCCCGCGCATCGTCTTAATGCACAGAAGCTGGAAAGCTCAGCTCGAAGAA
600
T A D P R I V P N A Q K L E K L S F E E
12 601
ATGCTGGAACTTGTGCTGGCTCAAGATTGGCTGCGCAGTGTGAAATACGCT
660
M L E L A A V G S K I V V L R S V E Y A
13 661
CGTGCATTCACTGTCGCACTTCGGTACGGCTCGTCTTATAGTANTGATCCGGCACTTGC
720
R A F N V P L R V R S S Y S N D P G T L
14 721
ATTGCCGGCTCATGGAGGATATTCTGTGGAAAGAAGCAGTCCTACCGGTGTGCAACC
780
I A G S M E D I P V E E A V L T G V A T
15 781
GACAAGTCCGAAGCCAAAGTAACCGTTCTGGGTATTCCGATAAGCCAGGGGAGGGCTGCC
840
D K S E A K V T V L G I S D K P G E A A

Fig 3A

290
114

REGISTRATION NO: 2
(CONT.)

Fig. 3B

Nucleotide sequence of ATCC21529 and (SEQ ID NO:2)

3
1 ATGACCACCA TCGCAGTTGT TGGTCCAACC GGCCAGGTCTG GCCAGGTAT
51 GCGCACCTT TTGGAAAGAGC GCAATTCCC AGCTGACACT GTTCGTTCT
101 TTGCATTCCCC GCGTTCCGCA GGCGCTAAGA TTGAATTCCG TGGCACGGAA
151 ATCGAGGTAG AAGACATTAC TCAGGCAACC GAGGAGTCCC TCAAGGGCAT
201 CGACGTTGCG TTGTTCTCTG CTGGAGGCAC CGCTTCCAAAG CAGTACGCTC
251 CACTGTTGCG TGCTGCAGGC GCGACTGTTG TGGATAACTC TTCTGCTTGG
301 CGCAAGGACG ACGAGGTCTC ACTAATCCTC TCTGAGGTGA ACCCTTCCGA
351 CAAGGATTCC CTGGTCAAGG GCATTATTGC GAATCCTAAC TGCACCCACCA
401 TGGCTGCAAT GCCAGTGCTG AAGCCACTGC ACGATGCCGC TGGCTTGTGTA
451 AAGCTTCACG TTTCCTCTTA CCAGGCTGTT TCCGGTTCTG GTCTTGCAAGG
501 TGTGGAAACC TTGGCAAAGC AGGTTGCTGC AGTTGGCGAC CACAACGTTG
551 AGTTCGTCCA TGATGGACAG GCTGCTGACCG CAGGCATGTC CGGACCTTAC
601 GTTTCCCCAA TCGCTTACAA CGTGTGCCA TTCGCGGGAA ACCTCGTCGA
651 TGACGGCACC TTCGAAACCG ACGAAGAGCA AAAGCTGCAC AACGAATCCC
701 GCAAGATTCT CGGCCTCCCA GACCTCAAGG TCTCAGGCAC CTGCGTCCGC
751 GTGCCGGTTT TCACCGGCCA CACCGTGAAC ATTCAACCCG AATTGACAA
801 GGCATTCACC GTCGAGGAGG CGCAGGAGAT CTTGGGTGCC GCTTCAGGCG
851 TCGAGCTTGT CGACGTCCTA ACCCCACTTG CAGCTGCCGG CATTGACGAA
901 TCCCTCGTTG GACGCATCCG TCAGGACTCC ACTGTCGACG ACAACCGCGG
951 TCTGGTTCTC GTCTGATCTG GCGATAACCT TCGCAAGGGC GCAGCACTGA
1001 ACACCATTCA GATTGCTGAG CTCTCGTTA AGTAA

Fig.4

SEQ. ID. No:4 amino acid sequence of ATCC 21579 and

ATGACCACCATGGCAGTTGGTGGTCAACCGGCCAGGTGGCCAGGTATGGCACCTT
1 -----+-----+-----+-----+-----+-----+-----+-----+ 60
M T T I A V V G A T G Q V G Q V H R T E
TTGGAGAGCGCAATTCCAGCTGACATGTTGCTTCCTGGCTCCGGCA
61 -----+-----+-----+-----+-----+-----+-----+-----+ 120
L E E R N F P A D T V R F F A S P R S A
GGCCGTAGATTGAATTCCGTCGCCACGGAAATCGAGGTAGAAAGACATTACTCAGGCAC
121 -----+-----+-----+-----+-----+-----+-----+-----+ 180
G R K I E F R G T E I E V E D I T O A T
GAGGACTCCCTAAGGGCATCGACGTTGGCTTCTCTGCTGGAGGCACCGCTCCARG
181 -----+-----+-----+-----+-----+-----+-----+-----+ 240
E E S L K G I D V A L E S A G G T A S K
CAGTACCGCTCCACTGTTTGCTGCTGCAGGCGGACTGTTGCTGGATAACTCTCTGCTTGG
241 -----+-----+-----+-----+-----+-----+-----+-----+ 300
Q Y A P L F A A N G A T V V V D N S S A W
CCGCAAGGACGAGGTTCACAAATCGCTCTGAGGTGAAACCTTCGACAAGGATTCC
301 -----+-----+-----+-----+-----+-----+-----+-----+ 360
R K D D E V P L I V S E V N P S O K D S
CTGGTCAGGGCATTTGGCAATCTTAATCTGACACCATGGCTGCAATGGCAGTGGCTG
361 -----+-----+-----+-----+-----+-----+-----+-----+ 420
L V K G I I A N P N G C T T H A A M P V L
AACCACTGCACGATGCCCTGGCTTGTAAAGCTTCACGTTCTTACCCACCGCTGT
421 -----+-----+-----+-----+-----+-----+-----+-----+ 480
K P L H D A A G L V U Z L H V S S Y Q A V
TCCGTTCTGGCTTGCAAGGTGTGCAACCTGGCAAGCAGGTGGCTGCAGTGGCGAC
481 -----+-----+-----+-----+-----+-----+-----+-----+ 540
S G S G L A C G V E T L A K Q V A A V G D
CACACACTGACTTCGCTCATGATGGACGCGCTGCTGACGGCAGGGATGTCGGACCTTAC
541 -----+-----+-----+-----+-----+-----+-----+-----+ 600
H N V E F V H O G Q R A D A G D V G P Y
GTTCCCCRATCGCTTACAAACGTCGCTGCCATTGGCGAAACCTCGCTGACGGCACC
601 -----+-----+-----+-----+-----+-----+-----+-----+ 660
V S P I A Y H V L P F A G N L V D U G T
ITCGAAACCGACGAAGAGCAGAAAGCTGCCAACGANTCCCGAAGATTCGGCCCTCCCA
661 -----+-----+-----+-----+-----+-----+-----+-----+ 720
F E T D E E Q K L R K E S R K I L G L P
CACCTCAAGGCTCAGGCACCTGGCTGGCTGCGGGTTTACCGGCCACACCGCTGAC
721 -----+-----+-----+-----+-----+-----+-----+-----+ 780
D L K V S G T C V R V P V E T G H T L T
ATTCAACGCCAACCTCGACAAGGCAATCACCGCTGACCGAGGGCAGGAGATCTGGCTGCC
781 -----+-----+-----+-----+-----+-----+-----+-----+ 840
I H A E F D K A I T V E O A Q E I L G A
GCTTCAGGCCGCTGAGCTTCGACGCTCCAAACCCACTTGCACCTGCCGCAATGACGAA
841 -----+-----+-----+-----+-----+-----+-----+-----+ 900
A S G V E L V O V S T P L A A G I O E

Fig 5A

SEQ ID NO:4
(Contd)

TCCCTCGTTGGA~~C~~GCATCCGTCAAGGACTCCACTGTCGACGACAACCGCGGTCTGGTTCTC
901 -----+-----+-----+-----+-----+-----+-----+-----+ 960
S L V G R I R Q D S T V D D N E G L V L
GTCGTATCTGGCGATAACCTTCGCAAGGGCGCAGCACTGAACACCATTCA~~G~~ATTGCTGAG
961 -----+-----+-----+-----+-----+-----+-----+-----+ 1020
V V S G D N L R K G A A L N T I Q I A E
CTGCTGGTTAAGTAA
1021 -----+----- 1035
L L V K *

F₅ 5β

Nucleotide sequence of dapA (SEQ ID NO:5)

1 ATGAGCACAG GTTTAACAGC TAAGACCGGA TAGAGCACT TCGGCACCGT
51 TGGAGTAGCA ATGGTTACTC CATTACCGA ATCCGGAGAC ATCGATATCG
101 CTGCTGGCCG CGAACGTCGCG GCTTATTGG TTGATAAGGG CTTGGATTCT
151 TTGGTTCTCG CGGGCACAC TGTTGAATCC CCAACGACAA CCGCCGCTGA
201 AAAACTAGAA CTGCTCAAGG CCGTTCTGTGA GGAAGTTGGG GATCGGGCGA
251 AGCTCATCGC CGGTGTCGGA ACCAACAAACA CGCGGACATC TTGTTGAACTT
301 GCGGAAGCTG CTGCTTCTGC TGGCCAGAC GGCTTTTAG TTGTAACTCC
351 TTATTAATCTCC AAGCCGAGCC AAGAGGGATT GCTGGCGCAC TTCTGGTCAA
401 TTGCTGCAGC AACAGAGGTT CCAATTGTC TCTATGACAT TTCTGGTCGG
451 TCAGGTATTC CAATTGAATC TGATACCATG AGACGCCGTGA GTGAATTACC
501 TACGATTTG GCGGTCAAGG ACGCCAAGGG TGACCTCGTT GCAGCCACGT
551 CATTGATCAA AGAAACGGGA CTTGCCTGGT ATTCAAGGCAGA TGACCCACTA
601 AACCTTGTTT GGCTTGCTTT GGGCGGATCA GGTTTCATTG CCGTAATTGG
651 ACATGCAGCC CCCACAGCAT TACGTGAGTT GTACACAAGC TTCTGGAGGAAG
701 GCGACCTCGT CGGTGCGCGG GAAATCAACG CAAACTATC ACCGCTGGTA
751 GCTGCCCAAG GTCGCTTGGG TGGAGTCAGC TTGGCAAAAG CTGCTcTGCG
801 TCTGCAGGGC ATCAACGTAG GAGATCCTCG ACTTCCAATT ATGGCTCCAA
851 ATGAGCAGGA ACTTGAGGCT CTCCGAGAAG ACATGAAAAA AGCTGGAGTT
901 CTATAA

Fig 6

SEQ FD NO: 6

as sequence
of dapt.

ATGACCAAGGTTTAAACGGTAAACGGAACTTGTCACGGTGGACTAGCA
60
M S T G L T A K T C V R H F G T V G V A
ATGGTTACTCCATTACCGGAATCCCGGAGACGCCATAACGCTTCTGCGCGAATCTCGG
61 ----- 120
H V T F F T E S A D I D I A I G P L I A
GCTTATTTGGCTGTGATAACCGCTTCTGCTTCTGCTGCGCGAATCTCGG
121 ----- 180
A Y L V D K G L D S L V L A C T T G E S
CCTACGACAAACGGCCGCTGAAAGACTAGAACTGCTCAAGGCCGTTCTGAGGAAGTTGGC
181 ----- 240
P T T T A A E K L E L L K A V R E E V G
GATCGGGCGAACGCTCATGCCCGTGTGGAAACCAACAAACACCGGGACATCTGTGGAACTT
241 ----- 300
D R A K L F A G V G T N N T R T S V E L
GCGGAAGCTGCTGCTCTGCTGCCGAGACGGCCCTTTAGTTGTAACTCCTTATTACTCC
301 ----- 360
A E A A A S A G A D E L L V V T P Y Y S
AAGCCGAGCCARGAGGGATTGCTGGCCACTTGGTGCATTTGCTGCAGCAACAGAGGTT
361 ----- 420
K P S Q E G L L A H F G A I K A A T E V
CCAATTGCTCTATGACATTCTGCTGGTCAAGTATTCGAATTGATCTGATACCATG
421 ----- 480
P I C L Y D I P G R S G : P T E S D T M
AGACCCCTGAGTGAATTACCTACCATTTGGCGGTCAAAGGACCTCAAGGGTGACCTCGTT
481 ----- 540
R R L S E L R T I L A V K D A K G D L V
GCAGCCACGGTCAATTGATCAAAGAAACGGGACTGGCTTGGTGGCGATGACCCACTA
541 ----- 600
A A T S L I K E T G L A K Y S C D D P L
AACCTTGTGGCTTGCTTGGCGGAACGGTTTCAATTGGCGTAATTGGACATGCAACCC
601 ----- 660
N L V H L A L G G S G F I S V I G H A A
CCCACAGCATTACCTGAGTTGACACAGCTTGGCGGAGGCGAACCTGCTGGCGCG
661 ----- 720
P T A L R E L Y T S T E E G I L V R A R
GAATCAACGSCAAACTATGACCGCTGGTAGCTGGCCAAAGGCTGGCTTGGTGAGCTCAGC
721 ----- 780
E I N A K G S P L V A R A Q G R A L G G V S
TTGGCAAAGCTGCTtCCGCTGCAAGGCGATCAACGCTAGGAGATCTGGACTTCCAAATT
781 ----- 840
L A K A A L R L Q G I H V G D P R L P I
ATGGCTCCAAATGACCAAGGAGACTTGAGGCTCTGGAGAARGACATGAAAAGCTGGAGTT
841 ----- 900
CTATAA
901 ----- 906

Fig 7

Nucleotide sequence of dapB (SEQ ID NO: 7)

```

  1 ATGGGAATCA AGGTTGGCGT TCTCCGAGCC AATGCCGTG TTGGTCACAC
  51 TATTGTGGCA GCAGTCATG AGTCCGACGA TCTGGAGCTT GTTGCAGAGA
  101 TCGGCCTCGA CGATGATTG AGCCTCTGG TAGACAACGG CGCTGAAGTT
  151 GTCGGTGAAT TCACCACTCC TAACCGCTGTG ATGGGCAACC TGGAGTTCTG
  201 CATCAACAAC GGCATTTCTG CGGTTGTTGG AACACACGGGC TTCGATAATG
  251 CTCGTTTGGA GCAGGTTCGC GcCTGGCTTG AAGGAAAAGA CAATGTCCGGT
  301 GTTCTGATCG CACCTAACTT TGCTATCTCT GCGGTGTTGA CCATGGTCTT
  351 TTCCAAGCAG GCTGCCCGCT TCTTGAATC AGCTGAAGTT ATTGAGCTGC
  401 ACCACCCCCAA CAAGCTGGAT GCACCTTCAG GCACCGCGAT CCACACTGCT
  451 CAGGGCATTG CTGCGGCACG CAAAGAAGCA GCATGGACG CACAGCCAGA
  501 TGGGACCGAG CAGGCACCTG AGGGTTCCCG TGGCGCAAGC GTAGATGGAA
  551 TCCCAGTTCA CGCAGTCCGC ATGTCCGGCA TGTTGCTCA CGAGCAAGTT
  601 ATCTTGGCA CCCAGGGTCA GACCTTGACC ATCAAGCAGG ACTCCTATGA
  651 TCGCAACTCA TTGACCCAG GTGTCTTGGT GGGTGTGCGC AACATTGCAC
  701 AGCACCCAGG CCTAGTCGTA GGACTTGAGC ATTACCTAGG CCTGTAA
  
```

Fig 8

SEQ ID NO: 8

Amino acid sequence of *dapB*

ATGGGAATCAAGGTTGGCGTTCTGGAGCCAAAGGCCGTGTTGGTCAAACATTGTGGCA
1 -----+-----+-----+-----+-----+-----+-----+-----+ 60
M G I K V G V L G A K G R V G Q T I V A
GCACTCAATGAGTCGACGATCTGGAGCTGTTGGAGATCGGGCTCGACGATGATTG
61 -----+-----+-----+-----+-----+-----+-----+-----+ 120
A V N E S D D L E L V A E I G V D D D L
AGCCTCTGGTAGACAACGGCGCTGAAGTGTGGTGAATTCAACCCTAACCGCTGTG
121 -----+-----+-----+-----+-----+-----+-----+-----+ 180
S L L V D N G A E V V V V D F T T P N A V
ATGGGCAACCTGGAGTTCTGCATCAACAACGGCATTCGCGGTGGAACCAACGGC
181 -----+-----+-----+-----+-----+-----+-----+-----+ 240
M G N L E F C I N N G I S A V V V G T T G
TTCGATAATGCTCGTTGGAGCAGGTTCGCGCTGGCTTGACCATGGCTTTCCAAGCAG
241 -----+-----+-----+-----+-----+-----+-----+-----+ 300
F D N A R L E Q V R A W L E G K D N V G
GTTCTGATCGCACCTAACCTTGCTATCTCTGCCTGACCATGGCTTTCCAAGCAG
301 -----+-----+-----+-----+-----+-----+-----+-----+ 360
V L I A P N F A I S A V L T M V F S K Q
GCTGCCCGCTTCTCGAATCAGCTGAAGTTATTGAGCTGCACCACCCAAACAAGCTGGAT
361 -----+-----+-----+-----+-----+-----+-----+-----+ 420
A A R F F E S A E V I E L H H P N K L D
GCACCTTCAGGCACCGCGATCCACACTGCTCAGGGCATGCTGCGGACGCAAAGCAAGCA
421 -----+-----+-----+-----+-----+-----+-----+-----+ 480
A P S G T A I H T A Q G I A A A R K E A
GGCATGGACGCACAGCCAGATGCGACCGAGCAGGCACTTGAGGGTCCCGTGGCGCAAGC
481 -----+-----+-----+-----+-----+-----+-----+-----+ 540
G M D A Q P D A T E Q A L E G S R G A S
GTAGATGGAATCCCAGTCACGCAGTCGGCATGTCCGGATGGTGCTCACGAGCAAGTT
541 -----+-----+-----+-----+-----+-----+-----+-----+ 600
V D G I P V H A V R M S G M V A H E Q V
ATCTTGGCACCCAGGGTCAGACCTTGACCATCAAGCAGGACTCCTATGATCGCAACTCA
601 -----+-----+-----+-----+-----+-----+-----+-----+ 660
I F G T Q G Q T L T I K Q D S Y D R N S
TTTGCACCAGGTCTGGGGTGTGGCAACATGCACAGCACCCAGGCCTAGTCGTA
661 -----+-----+-----+-----+-----+-----+-----+-----+ 720
F A P G V L V G V R N I A Q H P G L V V
GGACTTGAGCATTACCTAGGCCTGTAA
721 -----+-----+-----+-----+-----+-----+-----+-----+ 747
G L E H Y L G L *

Fig 9

Nucleotide. sequence of ddh (SEQ ID NO: 1)

```

1 ATGCATTCG GTAAGCTCGA CCAGGACAGT GCCACCACAA TTTTGGAGGA
51 TTACAAGAAC ATGACCAACA TCCGGTAGC TATCGTaGGC TACGGAACC
101 TGGGACCGAG CGTCGAAAAG CTTATTGCCA AGCAGCCCGA CATGGACCTT
151 GTAGGAATCT TCTCGCGCCG GGCCACCCCTC GACACAAAGA CGCCAGTCTT
201 TGATGTCGCC GACGTGGACA AGCACGCCGA CGACGTGGAC GTGCTGTTCC
251 TGTGCATGGG CTCCGCCACC GACATCCCTG AGCAGGCACC AAAGTTCCGCG
301 CAGTTCGCCT GCACCGTAGA CACCTACGAC AACCACCGCG ACATCCCACG
351 CCACCGCCAG GTCATGAACG AAGCCGCCAC CGCAGCCGGC AACGTTGCAC
401 TGGTCTCTAC CGGCTGGGAT CCAGGAATGT TCTCCATCAA CGCGTCTAC
451 GCAGCCGCAG TCTTAGCCGA GCACCGACAG CACACCTCTT GGGGCCAGG
501 TTTGTACAG GCCCCACTCCG ATGCTTTGCG ACCCATCCCT GGCAGTTCAA
551 AGGcGTCCA GTACACCCCTC CCATCCGAAG AaGCCCTGGG AAAGGCCGC
601 CGTGGCGAAG CCGGCGACCT CACCGGAAAG CAAACCCACA AGCGCCAATG
651 CTTCGTGGTT GCCGACGCGG CCGAcCACGA GCGCATCGAA AACGACATCC
701 GCACCATGCC TGATTACTTC GTTGGCTACG AAGTCGAAGT CAACTTCATC
751 GACGAAGCAA CCTTgGACgC CGAGCACACC GGCATGCCAC ACGGcGGaCA
801 CGTGATcACC ACCGGCGACA CCGGTGGCTT CAACACACCC GTGGAATACA
851 TCCTgAAGCT GGACCGAAAC CCAGATTCA CCCCTTCtTC ACAGATCGCT
901 TTCGGcCGCG CAGCTCACCG CATGAAGCAG CAGGGCCAAA GCGGtGCTTT
951 CACCGTCCTC GAAGTTGCTC CATACTGCT CTCCCCgGAG AACTTGGAtG
1001 ATCTGATCGC ACGCGACGTC TAA

```

Fig 10

SEQ ID 10: amino acid sequence of ddh.

SEQ ID
NO: 10

ATGTTTCTGTAAGTCGACCAAAAGTGCCACACACATTTCGGATTACAGAAC 60
M E F G F L D Q D S A T T I L E D Y K N
ATGCAACATCGCGCTACCTATCCTGGCTACGGAAAGCTGGACCCAGGTGGAAAAG 120
H T N I P V A I V G Y G H I C R S V E K
CTTATTGCCAAGCAGCCCCACATGGCTTGTAGGAATCTCTCCGGGGGGGACCCTC 180
121
L E A K Q P D M D L V G I F S R R A T E
GACACAAAGACCCAGTCTTGTGCGGACGTGGACAAGCACCCGACGTGGAC 240
181
D E K T P V E D V A D V D K H A D D V D
GTGCTGTTCTGTGCATGGCTCCCGACATCCCTGAGCAGGACCAAGTTGGCC 300
241
V L E L C H G S A T O I P E Q A P K E A
CAGTTGCCCTGACCGTAGACACCTACCGACAACCCACCGGACATCCACGCGACCCCGAG 360
301
O F A C T V D T Y D N H R D I P R H R Q
GTCATGAACGAAGCCGCCACCGCAGCCGCAACGTTGGACTGGTCTCTACCGEGCTGGGAT 420
361
V M N E A A T A A C N V A L V S T G H D
CCAGGAAATGTTCTCCATCAACCGCGTGTACCGAGGGCACTCTTAGCCGACACCCAG 480
421
P G M F S I N R V Y A A A V L A E H O Q
CACACCTTCTGGGGCCAGCTTGTACAGGGCACTCCGATCTTGGAGCATCCCT 540
481
H E F W G P G L S Q G H S D A L R R T P
GGCATTGAAAGGGCGTCCAGTACCCCTCCCATCCGAAGAAGCCCTGGCAACCGCCCGC 600
541
G V Q K A V D Y T L P S E E A L E H A R
CGTGCCTGAAACCCGGCACCTACCGGAAAGCAAACCCACAABGCCATGTTCTGGTT 660
601
R G E A G D L T G K Q T H K R O C F V V
CCCGACCGCGCGGACCGACCGACATCCAAACGACATCCGACCATCCCTATTTACTTC 720
661
A D A A D H E R I E N O I R T H E D Y E
GTTGGCTACGGAAAGTCGAACTTCATCGACGNACCTTGACGACCCACCCAC 780
721
V G Y E V E V N E I D E A T L D A E N T
GGCATGCCACACGGCGGACACGTGATEACCCACCGGACACCGGTGGCTTAAACACACCC 840
781
G M P H G G H V I T T C D T G C F H T
GTGGATACTCTGAAAGCTGGACCGANACCCAGATTTGACCCCTTCCTACAGATCCCT 900
841
V E Y I L K L D R N P D E T A S S Q I A
TTGGG=GGGGAGGCTCACCCATGAGCAGCAGGGCAAGGGGCGCTTACCCGTCCTC

Fig 11A

SEQ ID NO:10
(cont.)

901 F G R A A H R M K S Q C Q S G A F T V L
 GAAGTTGCTCCATACTTGCTCTCCCCGAGAGACTGGAtGATCTGATCGCAGCGAGGTC
 961 E V A P Y L L S P E N L D D L I A R D V
 TAA
 1021 --- 1023

Fig. II.B

Sequence of full length LysA from NRRL B-11474 (SEQ ID NO: 11); Underlined region: the priming site for lysA primer

ATGGCTACAGTGA~~AAA~~TTCAATGA~~ACT~~CCGCACACGTATGGCCACGCAATGCAGTG
CGCCAAAGACGGC~~T~~TGTCACCGTCGCTGGTGCGCTCTGCCCTGACCTCGCTGAAGAA
TACGGAA~~ACCC~~ACTGTT~~CGT~~AGTCGACGGAGGACGATTCCGTTCCGCTGCGGACATG
GCTACCGCATT~~CGT~~GGACCGGCAATG~~T~~GCACTACGCATCCAAAGCGTTCC~~T~~GACCAAG
ACCATTGCACGTTGGGTTGATGAAGAGGGCTGGCACTGGACATTGCGTCCATCAATGAA
CTGGCCATTGCCCTGGCCGCTGGTTCCGGCCACCGTATCACCGCGACGGCAACAAAC
AAAGGC~~T~~AGACTCC~~T~~GGCCGCTGGTCAAAACGGTGTCCGGCATG~~T~~GGTGC~~T~~GGAC
TCCGGCAGGAAT~~T~~GGAACT~~T~~GGATACGTTGCGCTGGTAAGGC~~A~~AGATCCAGGAC
GTGTTGATCCGGCTGAAGCCAGGTATCGAAGGCCACACCCACAGAGTTCATCGCCACTAGC
CACAGAACGACCAAGATTCGGATCTCCCTGGCATCGGTTCCGATTCGAAGCAGGCCAA
GCAGCCAACAA~~T~~CAGAGA~~ACT~~GAACCTGGTTGGCTGCACTGCCATGTTGGTTCCCAG
GTGTCGACGCCAAGGC~~T~~CAAGCTGGCAGAGGCCG~~T~~GGTGGGCTGTACTCACAG
ATCCACAGCGA~~ACT~~AGGTGTCC~~C~~TTCTGAGCTGGACCTCGGTGGG~~G~~ATA~~C~~GGCATC
GCC~~T~~ACACTG~~C~~AGATGAGGAAC~~A~~CTCAACGTCG~~C~~AGA~~G~~TGCGCTGGAGCC
GCAGTCGAAAAAATGGCAGCGGA~~ACT~~AGGCATCGACGCCACCAACCGTGC~~T~~GGTGGCC
GGCCGCCGCTATCC~~C~~AGGCCCTCCACCGT~~G~~ACCATCTACGAAGT~~T~~GGCACCACCAAAAC
GTCCACGTAGACGACGACA~~AA~~ACCCGCCCTACGTAGCCGTGACGGAGG~~G~~ATGTCCGAC
AACATCCGCCACCACTCTACGGCTCCGAATACGACGCCCGCGTAGTATCCGCTTGCC
GAAGGAGACCCAGTAAGC~~AC~~CCGCATCGTGGGCTCC~~C~~ACTGCGAATCCGGGATA~~T~~CC~~T~~
ATCAACGATGAAATCTACCCATCTGACATCACCAAGGGC~~G~~A~~T~~CC~~T~~CTCGC~~A~~CTCGCAGCC
ACCGGCCGATACTGCTACGCCATGAGCTCCGCTACACGCCITCACACGGCCCGCCCTC
GTGTCGCTCCGCCCTGGCAGCTCCGCCATGCTGGCCCGCGAACCCTGACGACATC
CTCTCACTAGAGGCATAA

Fig. 12

full length sequence of LysA (NRRL-B11474)
DIAMINOPIMELATE DECARBOXYLASE (Lys A) SEQ ID NO:12

MATVENFNEPAHVWPRNAVRQEDGVVTVAAGVPLPDLAEZYGTPLFVVDED
DPRSRCRM
ATAFGGEGCNHYASKAFLTKTIARWDEEGLALDTASINELGIALAAGFPASRITA
HGNN
KGVEFLRALVQNGVGHVVLDQAQELELLDYVAAGEGKIQDVLIRVKPGI
RAETTHEFIATS
HEDKRKGFSLASGSAYEAAKANNAENLNVLGHLCHVGSQVFDAEGFKLAAERVL
GLYSQ
IHSELGVALPELDLGGGYGIAYTADEEPLNVAEVASDLTAVGKMAELGIDAP
TIVLVEP
GRAIAGPSTVTTIYEVGTTKNVHDDDKTRRYVAVDGGMSDNIRPALYGSEY
DARVVSRFA
EGDPVSTRIVGSHCESGDILINDEIYPSDITSGDFLALAATGAYCYAMSS
RYNAFTRPAV
VSVRAGSSRIMLRRETLDLILSLEA

Fig. 13

Nucleotide

sequences of AS019 lysA (SEQ ID NO:13) (P RS6)

1 ATGGCTACAG TTGAAAATTT CAATGAACTT CCCGCACACG TATGGCCACG
51 CAATGCCGTG CGCCAAGAAG ACGGTTTGT CACCGTCGCT GGTGTGCCTC
101 TGCCTGACCT CGCTGAAGAA TACGGAACCC CACTGTCGT AGTCGACGAG
151 GACGATTCC GTTCCCCTG TGCGGACATG GCTACCGCAT TCGGTGGACC
201 AGGCAATGTG CACTACGCAT CTAAAGCGTT CCTGACCAAG ACCATTGCAC
251 GTTGGGTTGA TGAAGAGGGG CTGGCACTGG ACATTGCATC CATCAACGAA
301 CTGGGCATTG CCCTGGCCGC TGTTTCCCC GCCAGCCGTA TCACCGCGCA
351 CGGCAACAAC AAAGGCCTAG AGTTCTGCG CGCGTTGGTT CAAAACGGTG
401 TGGGACACGT GGTGCTGGAC TCCGCACAGG AACTAGAACT GTTGGATTAC
451 GTTGGCGCTG GTGAAGGCAA GATTCAAGGAC GTGTTGATCC GCGTAAAGCC
501 AGGCATCGAA GCACACACCC ACGAGTCAT CGCCACTAGC CACGAAGACC
551 AGAAGTCGG ATTCTCCCTG GCATCCGGT CCGCAATTGAA AGCAGCAAAA
601 GCCGCCAACAA CGCGAGAAAA CCTGAACTTG GTTGGCCTGC ACTGCCACGT
651 TGGTTCCCAAG GTGTTGACCG CCGAAGGCTT CAAGCTGGCA GCAGAACGCG
701 TGTTGGGCCT GTACTCACAG ATCCACAGCG AACTGGCGT TGCCCTTCCT
751 GAACTGGATC TCGGTGGCGG ATACGGCATT GCCTATAACCG CAGCTGAAGA
801 ACCACTCAAC GTCGCAGAAG TTGCCTCCGA CCTGCTCACCG CAGTCGGAA
851 AAATGGCAGC GGAACTAGGC ATCGACGCAC CAACCGTGCT TGTTGAGCCC
901 GGCCCGCCTA TCGCAGGCCCT CTCACCGTG ACCATCTACCG AAGTCGGCAC
951 CACCAAAGAC GTCCACGTAG ACGACACAA AACCCGCCGT TACATGCCG
1001 TGGACGGAGG CATGTCCGAC AACATCCGCC CAGCACTCTA CGGCTCCGAA
1051 TACGACGCCCG CGCTAGTATC CCGCTCGCC GAGGGAGACC CAGTAAGCAC
1101 CCGCATCGTG GGCTCCCACT GCGAAATCCGG CGATATCCTG ATCAACGATG
1151 AAATCTACCC ATCTGACATC ACCAGTGGCG ACTTCCTTGC ACTCCGAGCC
1201 ACCGGCGCAT ACTGCTACGC CATGAGCTCC CGCTACAAACG CCTTCACACG
1251 GCCCGCCGTC GTGTCCGTCC GCGCTGGCAG CTCCCGCCTC ATGCTGCGCC
1301 GCGAAACGCT CGACGACATC CTCTCACTAG AGGCATAA

Fig. 14

SEQ ID NO: 14 Full length amino acid sequence of LysA (pRS6)

```

ATGGCTACAGTTGAAAATTCAATGAACTTCCCGCACCGTATGCCACGGCCTGCCGTG
1. -----+-----+-----+-----+-----+-----+-----+-----+-----+ 60
M A T V E N F N E L P A H V W P R K A V
CGCCAAGAACGGCGTTGTCACCCTCGTGGTGTGCCCTGCCCTGACCTCGCTGAAGAA
61 -----+-----+-----+-----+-----+-----+-----+-----+ 120
R Q E D G V V T V A G V P L P D L A E E
TACGGAACCCCACGTTCGTAGTCGACGAGGACGATTCCGTTCCGCTGTCGCACATG
121 -----+-----+-----+-----+-----+-----+-----+-----+ 180
Y G T P L F V V D E D D F R S R C R D M
GCTACCGCATTGGTGGACCAGGCAATGTGCACTACGCATCTAAAGCGTTCCGTGACCAAG
181 -----+-----+-----+-----+-----+-----+-----+-----+ 240
A T A F G G P G N V H Y A S K A F L T K
ACCATTGCACGTTGGGTTGATGAAGAGGGGCTGGCACTGGACATTGCATCCATCAACGAA
241 -----+-----+-----+-----+-----+-----+-----+-----+ 300
T I A R W V D E E G L A L D I A S I N E
CTGGGCATTGCCCTGGCCGCTGGTTCCCGCCAGCGTATCACCGCGCACGGCAACAAAC
301 -----+-----+-----+-----+-----+-----+-----+-----+ 360
L G I A L A A G F P A S R I T A H G N N
AAAGGCCTAGAGTTCCCTGCCGCGCTGGTTCAAACGGTGTGGGACACGTGGTCCGTGGAC
361 -----+-----+-----+-----+-----+-----+-----+-----+ 420
K G V E F L R A L V Q N G V G H V V L D
TCCGCACAGGAACTAGAACTGTTGGATTACGTTGCCGCTGGTGAAGGCAAGTTCAAGGAC
421 -----+-----+-----+-----+-----+-----+-----+-----+ 480
S A Q E L E L L D Y V A A G E G K I Q D
GTGTTGATCCCGTAAAGCCAGGCATCGAACACACCCACCGAGTTCATGCCACTAGC
481 -----+-----+-----+-----+-----+-----+-----+-----+ 540
V L I R V K P G I E A H T H E F I A T S
CACGAAGACCAAGAAGTCGGATTCTCCCTGGCATCCGGTCCGATTGAAAGCAGCAAAA
541 -----+-----+-----+-----+-----+-----+-----+-----+ 600
H E D Q K F G F S L A S G S A F E A A K
GCCGCCAACAAACGCAAGAAAACCTGAACCTGGTGGCCTGCAC TGCCACGTTGGTCCAG
601 -----+-----+-----+-----+-----+-----+-----+-----+ 660
A A N N A E N L N L V G L H C H V G S Q

```

Fig 15A

SEQ ID NO: 14 Lys A (β RS6)
 (cont'd)

```

  GTGTTGACGCCGAAGGCTTCAAGCTGGCAGCAGAACCGGTGTTGGGCCTGTACTCACAG
  661. -----+-----+-----+-----+-----+-----+ 720
      V F D A E G F K L A A E R V L G L Y S Q

  ATCCACACCGGAACTGGCGTTGCCCTTCTGAACCTGGATCTCGGTGGCGGATACGGCATT
  721 -----+-----+-----+-----+-----+-----+ 780
      I H S E L G V A L P E L D L G G G Y G I.

  GCCTATAACCGCAGCTGAAGAAGCACTAACGTCGCAGAAGTTGCCTCCGACCTGCTCACC
  781 -----+-----+-----+-----+-----+-----+ 840
      A Y T A A E E F L N V A E V A S D E L T

  GCAGTCGGAAAAATGGCAGCGGAACCTAGGCATCGACGCCAACCGTGTTGAGGCC
  841 -----+-----+-----+-----+-----+-----+ 900
      A V G K M A A E L G I D A P T V L V E P

  GGCGCGCTATCGCAGGCCCTCCACCGTGACCATCTACGAAGTCGGCACCAAGAC
  901 -----+-----+-----+-----+-----+-----+ 960
      G R A I A G P S T V T I Y E V G T T K D

  GTCCACGTAGACGACCAAAACCCGCCCTACGCCGTGGACCGAGGCATGTCCGAC
  961 -----+-----+-----+-----+-----+-----+ 1020
      V H V D D D K T R R Y I A V D G G M S D

  AACATCCGCCAGCACTCTACGGCTCCGAATACGACGCCCGTAGTATCCCCTCGCC
  1021 -----+-----+-----+-----+-----+-----+ 1080
      N I R P A L Y G S E Y D A R V V S R F A

  GAAGGAGACCCAGTAAGCACCCGCATCGTGGCTCCACTGCGAATCCGGCGATATCCG
  1081 -----+-----+-----+-----+-----+-----+ 1140
      E G D P V S T R I V G S H C E S G D I L

  ATCAACGTGAATCTACCCATCTGACATACCAGCGGCGACTTCCTGCACTCGCAGCC
  1141 -----+-----+-----+-----+-----+-----+ 1200
      I N D E I Y P S D I T S G D F L A L A A

  ACCGGCGCATACTGCTACGCCATGAGCTCCCGCTACAAACGCCCTCACACGGCCCGCCGTC
  1201 -----+-----+-----+-----+-----+-----+ 1260
      T G A Y C Y A M S S R Y N A F T R P A V

  GTGTCCGTCCGCCCTGGCAGCTCCCGCTCATGCTGCGCCGCAAACGCTCGACGACATC
  1261 -----+-----+-----+-----+-----+-----+ 1320
      V S V R A G S S R L M L R R E T L D D I
  
```

Fig 15B

S₂O₄ ID No: 14 Lys A (P_{RS6})
(cont.)
CTCTCACTAGAGGCATAA
1321 ----- 1338
L S L E A

Fig 15C

Nucleotide. sequence of orf2 in dapB operon SEQ ID NO: 15

1 GTGGCCGAAC AAGTTAAATT GAGCGTGGAG TTGATAGCGT GCAGTTCTT
51 TACTCCACCC GCTGATGTTG AGTGGTCAAC TGATGTTGAG GCGCGGAAAG
101 CACTCGTCGA GTTTGCGGGT CGTGCCTGCT ACGAAACTTT TGATAAGCCG
151 AACCCCTCGAA CTGCTTCCAA TGCTCGGTAT CTGCGCCACA TCATGGAAGT
201 GGGGCACACT GCTTTGCTTG AGCATGCCA TGCCACGATG TATATCCGAG
251 GCATTTCTCG GTCCGCGACC CATGAATTGG TCCGACACCG CCATTTTCC
301 TTCTCTAAC TGTCTCAGCG TTTCTGTGCAC AGCGGAGAAT CGGAAGTAGT
351 GGTGCCCCACT CTCATCGATG AAGATCCGCA GTTGCCTGAA CTTTTCATGC
401 ACGCCATGGA TGAGTCTCGG TTGCTTTCA ATGAGCTGCT TAATCCGCTG
451 GAAGAAAAAC TTGGCGATGA ACCGAATGCA CTTTTAAGGA AAAAGCAGGC
501 TCGTCAAGCA GCTCGCGCTG TGCTGCCAA CGCTACAGAG TCCAGAATCG
551 TGGTGTCTGG AAACCTCCGC ACCTGGAGGC ATTTCATTTGG CATGCGAGCC
601 AGTGAACATG CAGACGTCGA AATCCGCGAA GTAGCGGTAG GATGTTTAAG
651 AAAGCTGCAG GTAGCAGCGC CAACTGTTT CGGTGATTTT GAGATTGAAA
701 CTTTGGCAGA CGGATCGCAA ATGGCAACAA GCGCGTATGT CATGGACTTT
751 TAA

Fig 1b

SEQ ID No: 16

ORF2 amino acid sequence

GTGGCCGAACAAAGTTAAATTGAGCGTGGAGTTGATAGCGTGCAGTTCTTTACTCCACCC
1 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 60
M A E Q V K L S V E L I A C S S F T P P
GCTGATGTTGAGTGGTCAACTGATGTTGAGGGCGCGAACGACTCGTCGAGTTGCAGGT
61 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 120
A D V E W S T D V E G A E A L V E F A G
CGTGCCTGCTACGAAACTTTGATAAGCCGAACCCCTCGAACTGCTTCCAATGCTGCGTAT
121 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 180
R A C Y E T F D K P N P R T A S N A A Y
CTGCGCCACATCATGGAAGTGGGGCACACTGCTTGCTTGAGCAGGCCATGCCAACGATG
181 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 240
L R H I M E V G H T A L L E H A N A T M
TATATCCGAGGCATTCTCGGTCCCGCACCATGAATTGGTCCGACACCGCCATTTC
241 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 300
Y I R G I S R S A T H E L V R H R H F S
TTCTCTCAACTGTCTCAGCGTTCGTGACAGCGGAGAACGAAAGTAGTGGTGCCTACT
301 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 360
F S Q L S Q R F V H S G E S E V V V P T
CTCATCGATGAAGATCCGCAGTTGCGTAACCTTCATGCACGCCATGGATGAGTCTCGG
361 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 420
L I D E D P Q L R E L F M H A M D E S R
TTCGCTTCATGAGCTGCTTAATGCGCTGGAAAGAAAAACTTGGCAGAACCGAATGCA
421 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 480
F A F N E L L N A L E E K L G D E P N A
CTTTTAAGGAAAGCAGGCTCGCAAGCAGCTCGCGCTGTGCTGCCAACGCTACAGAG
481 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 540
L L R K K Q A R Q A A R A V L P N A T E
TCCAGAACATGCGGGCTCTGGAAACTCCGCACCTGGAGGCATTCATTGGCAGTCGAGCC
541 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 600
S R I V V S G N F R T W R H F I G M R A
AGTGAACATGCAAGACGTCGAATCCCGAAGTAGCGTAGGATCTTAAGAAAGCTGCAG
601 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 660
S E H A D V E I R E V A V G C L R K L Q
GTAGCAGCGCCAACATGTTTGGTGAATTGAGATTGAAACTTGGCAGACGGATCGCAA
661 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 720
V A A P T V F G D F E I E T L A D G S Q
ATGGCAACAAGCCCGTATGTCATGGACTTTAA
721 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 753
M A T S P Y V M D F *

fig 17

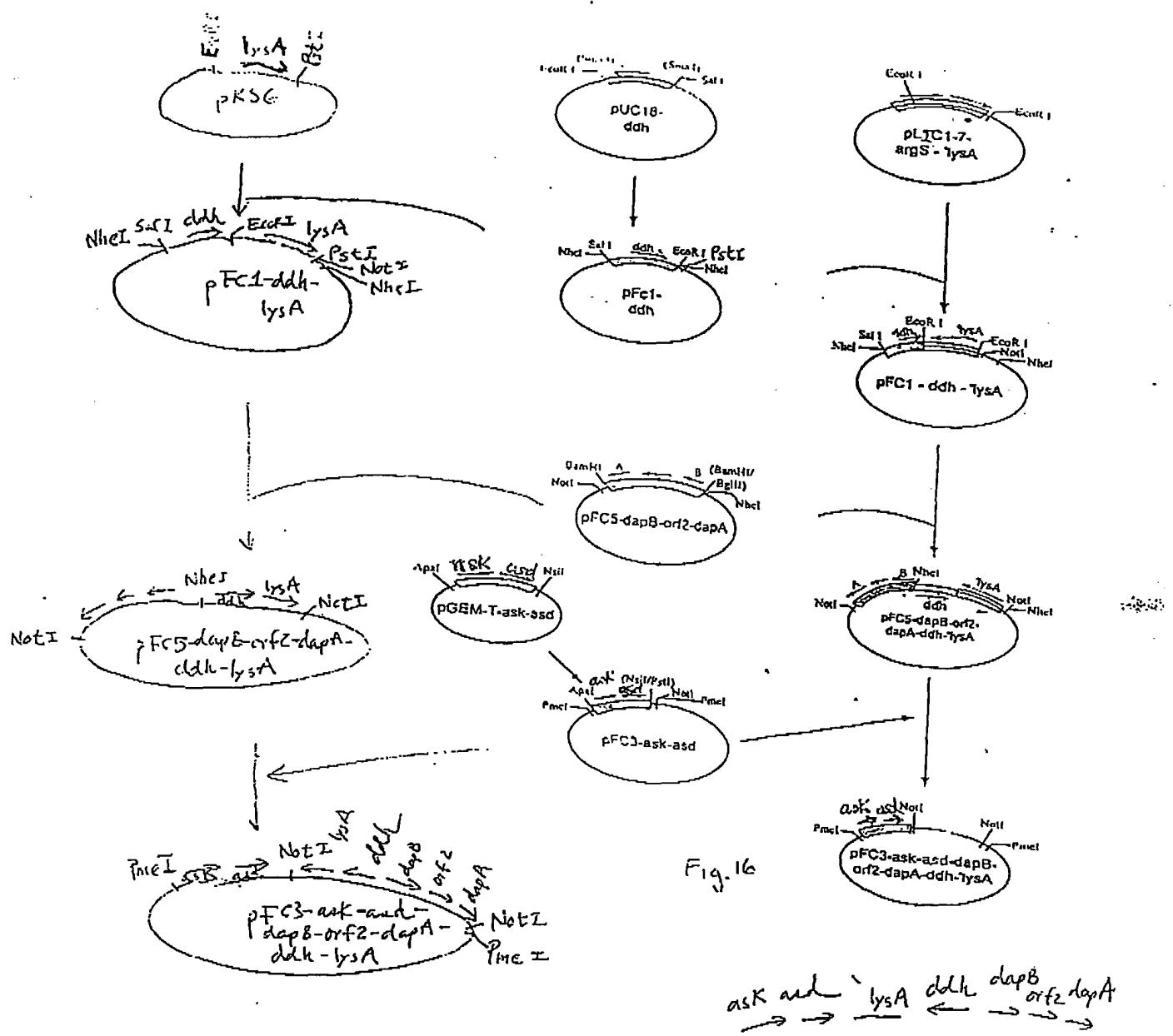


Fig. 18

ask asc → lysA ddh dapB orf2 dapA

DRAFT ALIGNMENT

ATCC 13032		50
N13		
ATCC 21529		
Consensus	MALVVQKYGG SSLESAERIR NVAERIVATV KAGNDVVVC SAKGDTTDEL	
	V	
	C	
	C	
ATCC 13032	51	100
N13		
ATCC 21529		
Consensus	LELAAAVNPV PPAREMDMLL TAGERISNAL VAMAIESTLG EAQSFTGSQA	
ATCC 13032	101	150
N13		
ATCC 21529		
Consensus	GVLTTERHGN ARIVDVTPGR VREALDEGKI CIVAGFQGVN KETRDVTTLG	
ATCC 13032	151	200
N13		
ATCC 21529		
Consensus	RGGSDTTAVA LAAALNADVC EIYSOVDGVY TADPRIVPNA QYLEKLSFEE	
ATCC 13032	201	250
N13		
ATCC 21529		
Consensus	MLELAAVGSK ILVLRSEYEA RAFNVPLRVR SSYSNDPCTL IAGSMEDIPV	
ATCC 13032	251	300
N13		
ATCC 21529		
Consensus	EEAVLTGVAT DKSEAKVTVL CISDKPGEAA KVFRALADEE IXIDMVLQNV	
ATCC 13032	301	350
N13	S	
ATCC 21529	A	G
Consensus	SSVEDGTTDI TFTCPRADGR RAMEILKKLQ VQGNWTNVLY DQ2VGHVSLV	D
	A	G
ATCC 13032	351	400
N13	T	
ATCC 21529	T	
Consensus	GAGMKSHPGV TAEFMEALRD VNVIELIST SEIRISVLIR EDDLOAAARA	I
ATCC 13032	401	421
N13		
ATCC 21529		
Consensus	LHEQFQLGGE DEAVVYACTG R	

Fig. 19

*Hpa*I - *Pvu*II fragment comprising the P1 promoter

AACCGGTGTGGAGCCGACCATTCCCGAGGCCTGCACTGCAACGAGGTCTAGTTTGGTACATGGCTTCTG
GCCAGTTCATGGATTGGCTGCCGAAGAAAGCTATAAGGCATGCCACCAAGGGCACCAGGAGITACCGAAGAT
GGTGCCGTGCTTTGCCCTGGGCAGGGACCTTGACAAAGCCCACGCTGATATGCCAAGTGAAGGGATCAG
AATAGTGCATGGGACGTGGATGCTGCCACATTGAGCGGAGGCATATCTACCTGAGGTGGGCATTCTCC
CAGCGGATGTTCTGCGCTGCTGCAGTGGGCATTGATACCAAAAAGGGGCTAACGCGACTCGAGGCCG
CAAGAACTGCTACTACCTTTTATTGTCGAACGGGCATTACGGCTCCAAGGACGTTGTTCTGGTCA
GTTACCCAAAAAGCATATAACAGAGACCAATGATTTCATTAAAAAGGCAGGGATTGTTATAAGTATGG
GTCGTATTCTGTGGCACGGGTGTACCTCGGCTAGAATTCTCCCCATGACACCAG

Fig. 20 (SEQ ID NO: 17)

Making pFC1-ddh-lysA

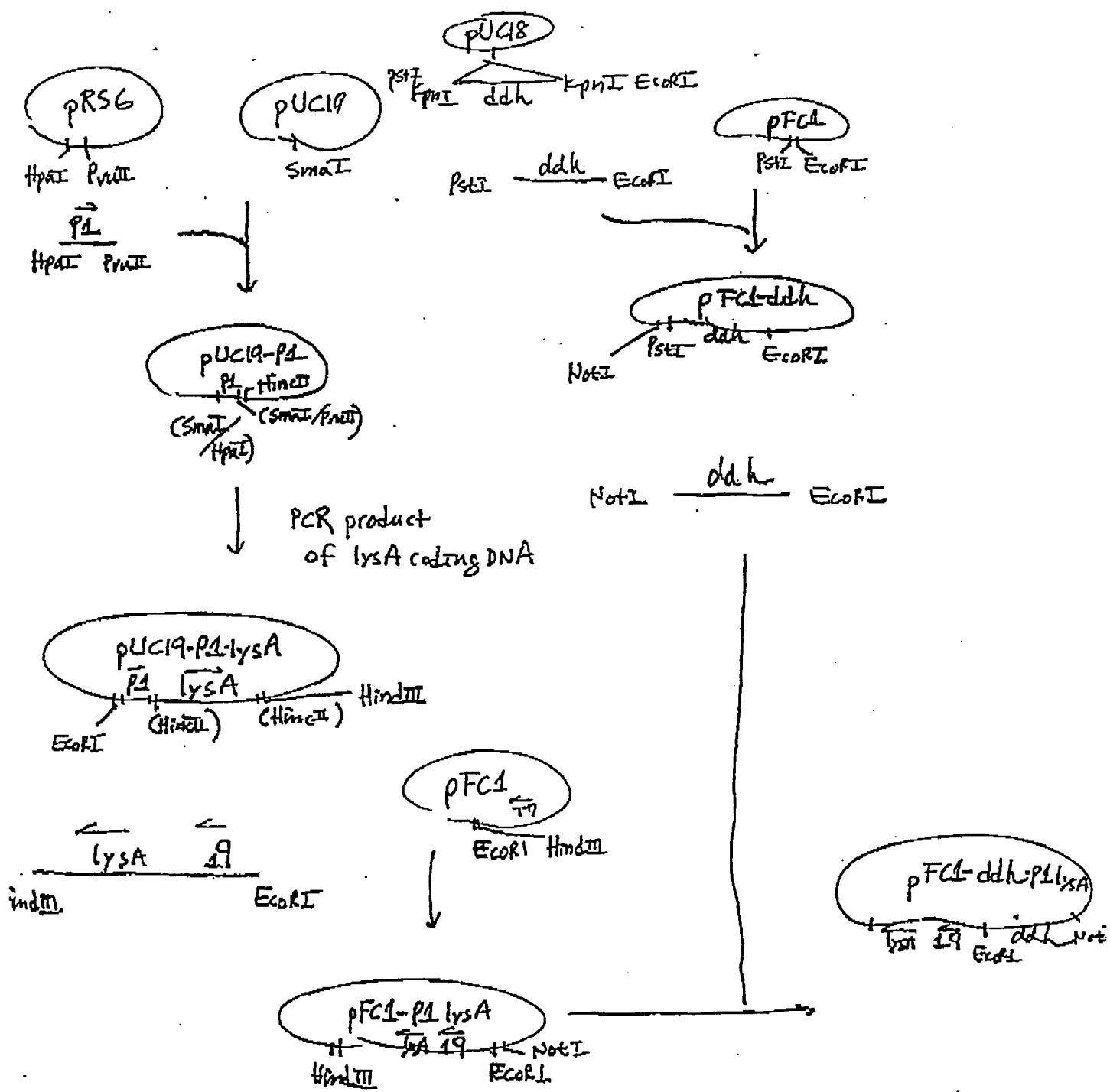
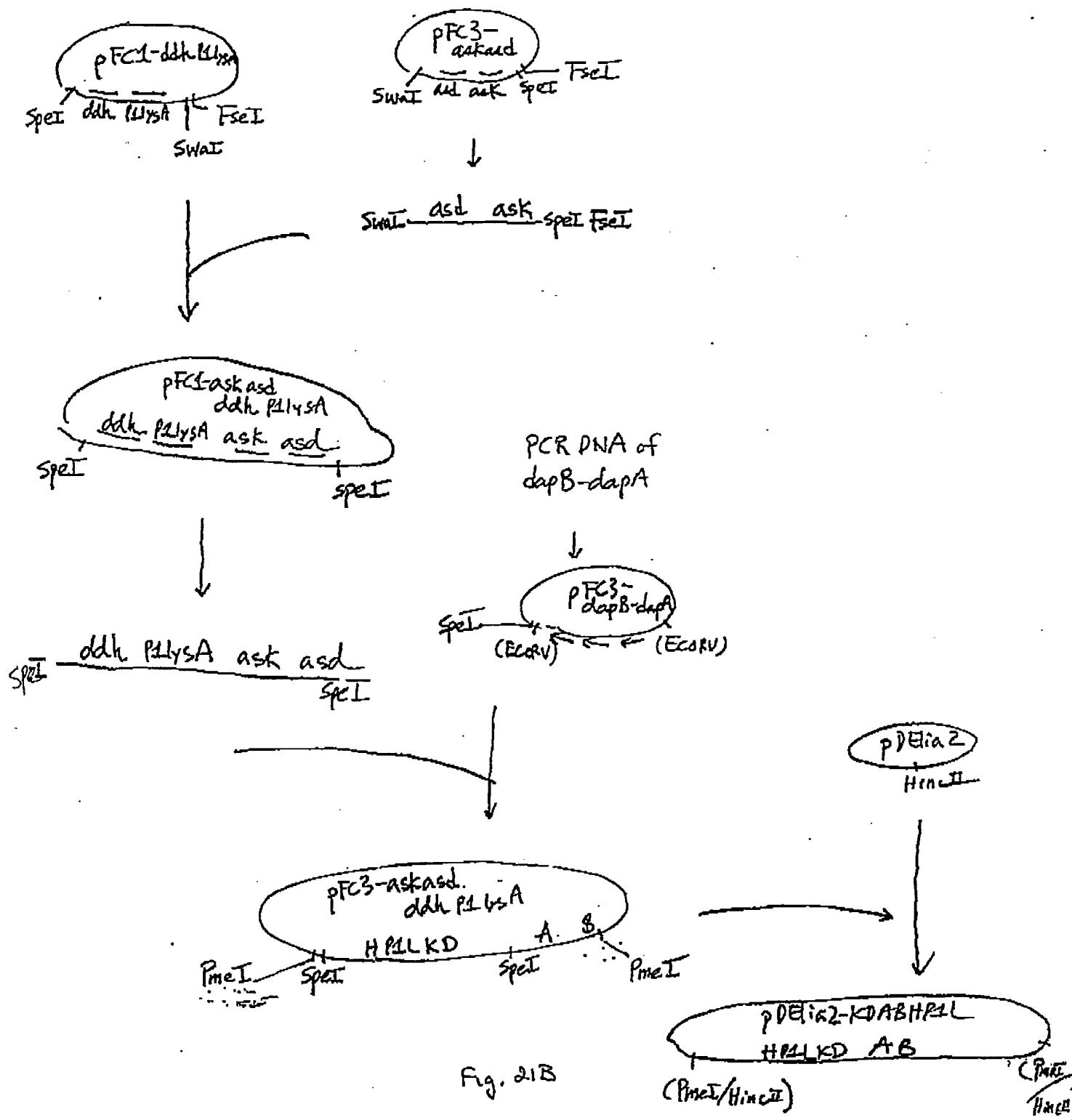
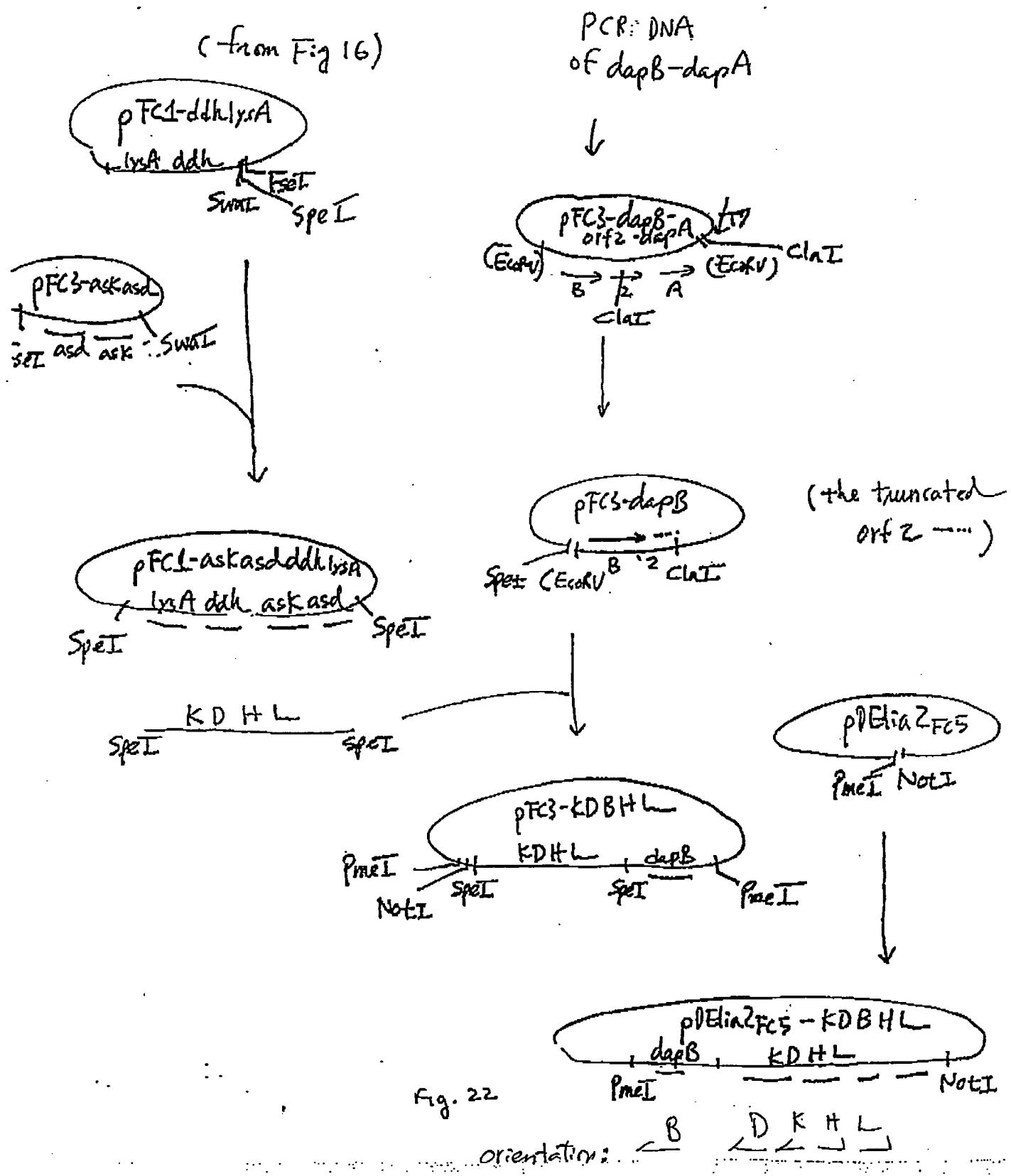


Fig. 21A

Making pDElia2-KDABHP1L



Making pDElia2_{FC5}-KDBHL



nucleotide sequence of truncated ORF2

SER ID No: 18

1 GTGGCCGAAC AAGTTAAATT GAGCGTGGAG TTGATAGCGT GCAGTTCTT
51 TACTCCACCC GCTGATGTTG AGTGGTCAAC TGATGTTGAG GGCAGCGGAAG
101 CACTCGTCGA GTTTGCGGGT CGTGCCTGCT ACGAAACTTT TGATAAGCCG
151 AACCCCTCGAA CTGCTTCCAA TGCTGCGTAT CTGCGCCACA TCATGGAAGT
201 GGGGCACACT GCTTTGCTTG AGCATGCCAA TGCCACGATG TATATCCGAG
251 GCATTTCCTCG GTCCGGGACCC CATGAATTGG TCCGACACCG CCATTTTCC
301 TTCTCTCAAC TGTCTCAGCG TTTCGTGCAC AGCGGAGAAT CGGAAGTAGT
351 GGTGCCCACT CTCAT

Fig. 23

SEQ. ID. NO: 19

Truncated ORF-2

amino acid sequence

GTGGCCGAACAAGTTAAATTGAGCGTGGAGTTGATAGCGTCAGTTCTTTACTCCACCC
1 -----+-----+-----+-----+-----+-----+-----+-----+ 60
M A E Q V K L S V E L I A C S S F T P P
GCTGATCTTGACTGGTCAACTGATGTTGAGGGCGCGAACGACTCGTCGAGTTGCGGGT
61 -----+-----+-----+-----+-----+-----+-----+-----+ 120
A D V E W S T D V E G A E A L V E E F A G
CGTGCCCTGCTACGAAACTTTGATAAGCCGAACCCCTCGAACTGCTTCCAATGCTGCGTAT
121 -----+-----+-----+-----+-----+-----+-----+-----+ 180
R A C Y E T F D K P N P R T A S N A A Y
CTGCGCCACATCATGGAAAGTGGGGCACACTGCTTGCTTGAGCATGCCAATGCCACGATG
181 -----+-----+-----+-----+-----+-----+-----+-----+ 240
L R H I M E V G H T A L L E H A N A T M
TATATCCGAGGCATTCTCGGTCCGCGACCCATGAATTGGTCCGACACCGCCATTTC
241 -----+-----+-----+-----+-----+-----+-----+-----+ 300
Y I R G I S R S A T H E L V R H R H F S
TTCTCTCAACTGTCTCAGCGTTCTGCACAGCGGAGAATCGGAAGTAGTAGTGGTCCCCACT
301 -----+-----+-----+-----+-----+-----+-----+-----+ 360
F S Q L S Q R F V H S G E S E V V V P T
CTCAT ...
361 -----

L (I)

fig. 24

SEQ ID NO: 20

Sequence of truncated Lys A (LysA) (NRL-B11474)

ATGGCTACAGTTGAAATTCAATGAACCTCCGCACACGTATGCCACGCAATCAGTG
CGCCAAGAAGAOGGCGTTGTCACCGTCGCTGGTGTGCCCTGCCCTGACCTCGCTGAAGAA
TACGGAACCCCACITGTTGCTAGTCGACGGAGGACGATTCCGTTCCCGCTGTCGGCACATG
GCTACCGCATCGGTGGACAGGCAATGTGCACTACGCATCCAAAGCGTTCCCTGACCAAG
ACCATTGCAACGTTGGGTGATGAAGAGGGCTGGCACTGGACATTGCGTCCATCAATGAA
CTGGGCATTGGCTTGGCCGCTGGTTTCCCGCAGCCGTATCACCGCAGGGCAACAAC
AAAGGCGTAGAGTTCTGGCGCGTTGGTTCAAACGGTGTGGCATGTGGTGCTGGAC
TCCGGCCAGGAATTGGAACTGCTGGATTACGTTGGCGTGGTAAGGGAAAGATCCAGGAC
GTGTTGATCCCGTGAAGCCAGGTATCGAAGCCCACACCCACQAGTTCATGCCACTAGC
CACGAAGACCAAGAAGTTGGATTCTCCCTGGCATCCGGTTCCGCATTGAAAGCAGCGAAA
GCAGCCAACAAATGCAGAGAACTTGAACCTGGTTGGTCTGCACGTGCCATGTTGGTCCAG
GTGTTGCAAGCCGAAGGCTTCAAGCTGGCAGCAGAGCGCGTGTGGGCTGTACTCACAG
ATCCACAGCGAACTAGGTGTCGCCCTTCTGAGCTGGACCTCGGTGGGGATAACGGCATT
GCCTACACTGCGAGATGAGGAACCACTCAACGTCGCAGAAGTCGCCCTCCGACCT

Fig. 25

Truncated sequence of LysA (NRRL-B11474)
DIAMINOPIMELATE DECARBOXYLASE (Lys A) seq id: 21

MATVENFNEI.PAHVWPRIAVRQEDGVITVAGVPLPDLAEYGTPLFVVDEDDFRSRCRM
ATAFGCGGNVHYASKARLTITIARMVDEEGLALDTASINELGIALAAGFPASRITAHCNN
KGVEFLRALVQNCVGHVVLDSAQEELLIDYVAAGEGKIQDVLIRVKPGIEAHTHEFIATS
HEDQKFGFSLASGSafeAAKAANNAENLNLVGLRCHVGSQVFDAEGFKLAERVLGLYSQ
IHSSELGVALPELDLGGGYGIAYTADEEPLNVAEVASDL

Fig. 26